IN THE UNITED STATES DISTRICT COURT
FOR THE NORTHERN DISTRICT OF OKLAHOMA

STATE OF OKLAHOMA, et al. Plaintiffs, v. TYSON FOODS, INC., et al. Defendants.	)	Case No. 4:05-cv-00329-GKF-PJC

REPLY IN SUPPORT OF DEFENDANTS' MOTION TO EXCLUDE EXPERT TESTIMONY BASED ON BACTERIAL ANALYSES CONDUCTED IN VIOLATION OF EPA, USGS AND OKLAHOMA STANDARDS (Dkt. No. 2090)

Exhibit 1

Declaration of Myoda and Samadpour

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STATE OF OKLAHOMA, ex rel. W.A. DREW EDMONDSON, in his capacity as ATTORNEY GENERAL OF THE STATE OF OKLAHOMA AND OKLAHOMA SECRETARY OF THE ENVIRONMENT C. MILES TOLBERT, in his capacity as the TRUSTEE FOR NATURAL RESOURCES FOR THE STATE OF OKLAHOMA **PLAINTIFFS**

v. **CASE NO.: 05-CV-00329 GKF –SAJ**

TYSON FOODS, INC., TYSON POULTRY, INC., TYSON CHICKEN, INC., COBB-VANTRESS, INC., CAL-MAINE FOODS, INC., CAL-MAINE FARMS, INC. CARGILL, INC., CARGILL TURKEY PRODUCTION, LLC, GEORGE'S, INC., GEORGE'S FARMS, INC., PETERSON FARMS, INC., SIMMONS FOODS, INC. and WILLOW BROOK FOODS, INC. **DEFENDANTS**

Declaration of Dr. Mansour Samadpour and Dr. Samuel P. Myoda

1. Dr. Mansour Samadpour is President of IEH Laboratories and Consulting Group and Molecular Epidemiology, Inc. (IEH). Dr. Samuel Myoda is Vice President of IEH. Our CVs are attached hereto as Exhibit 1 and 2. In the last four years, Dr. Samadpour has testified in the following cases:

   Novak v. Kroger Co. of Michigan, 02-038264-NP (Mich. Cir. Ct.)

   Bar-S Foods v. Tiromat, et al., CJ-02-111 (Okl. Dist. Ct.)

   Metz v. Dalesio's of Lilttle Italy, 24-C-06-001426OT (Baltimore Cir. Ct.)

2. IEH was retained in November of 2007 by Defendants at an hourly rate of $400/hr for Dr. Samadpour and $350 for Dr. Myoda to serve as expert consultants regarding, but not limited to, microbial source tracking, microbiology, water quality, public health and related regulatory affairs. We have been asked to review the Plaintiff's testimony, the water quality data and other relevant parameters that influence water quality in the Illinois River Watershed (IRW) and to offer our scientific opinions on the water quality and factors that affect the water quality in the IRW.

3. Bacteria are microscopic, unicellular organisms that are prokaryotes, meaning that unlike our cells they do not contain a nucleus. There are many different physical and biological properties of these organisms, they have preferred habitats, and interact with their surroundings in many different ways. There are literally trillions upon trillions of bacteria in the environment and the overwhelming majority of them are not pathogenic. Bacteria are an integral part of our lives; they are used in food production, e.g. yogurt and cheese, in our digestive system, e.g. *E. coli* and enterococcus, in the soil, e.g. nitrogen fixing bacteria that are essential to the nutrient cycle and are also in the air and water. Bacteria are used to treat wastewater, to break down pollutants, e.g. bioremediation, and are used in drug development and production. There are a plethora of beneficial uses for bacteria.

4. Despite the wealth of knowledge regarding bacteria, in fact relatively little is known about the total universe of bacteria, and it is estimated that scientists have been able to culture (grow in the lab) < 2% of the bacteria that exist. There are a host of factors that affect the "fate and transport" of specific types of bacteria in the environment: how do different bacteria handle different environmental factors; what is the relationship between bacterial transport and

precipitation; what factors govern soil infiltration and filtration/sorption; what characteristics govern relative survival rates, predation rates, and growth rates; and the impact of factors such sunlight (UV radiation), temperature, sedimentation, humidity, pH, moisture content, etc.? These factors affect the fate and transport of each bacterium.

5. Developing strategies to protect public health has driven the study of microbiology. In the late 1800s/early 1900s, illness due to poor sanitation and water quality was commonplace, largely due to inadequate sewage treatment, hence the need to develop and install sewage treatment facilities and limit, if not prevent, fecal matter from entering the water. In order to evaluate the effectiveness of the treatment interventions and resulting water quality, a test was needed. The ideal approach is to test for the pathogens in the water directly; however, many of the pathogens were unknown, in relatively small quantities and hard if not impossible to test for at the time. Therefore, the indicator organism approach was embraced and because certain coliforms are virtually always found in feces, the presence of total coliforms was used as an indication that fecal contamination was probable. The total coliform group contains bacteria such as Citrobacter, Enterobacter, Escherichia (*E. coli*), Hafnia, Klebsiella, Serratia and Yersinia.

6. The problem with using total coliforms as an indicator of fecal contamination is that not all the bacteria in this group are found in feces. In an effort to increase the accuracy of the indicator organism approach, a subset of total coliforms – the faecal coliform group (aka fecal coliform) replaced total coliforms as a measure of water quality. The faecal coliform group contains bacteria such as *E. coli*, Citrobacter, Enterobacter and Klebsiella. Although this was a better approach, it still did not eliminate the possibility that indicators would be found when in fact there was no fecal contamination (or pathogens) present. This is because in the faecal coliform

group, *E. coli* is associated with feces however; organisms such as Citrobacter, Enterobacter and Klebsiella do not originate in feces and because the faecal coliform count does not differentiate which bacteria(s) are being quantified, it is not known which organisms are present/absent or where they came from.

7. In the early 1980s, realizing the shortcomings of the use of faecal coliforms as an indicator, the EPA set out to develop a better methodology to measure water quality. The technology was still not in place to directly detect all the potential pathogens so alternative indicator bacteria were evaluated. By definition, indicator(s) must be easy to detect, non pathogenic, exist in greater quantities than the pathogen and must live longer than the pathogens. An indicator would be useless if it did not persist in the environment at least as long as the pathogen. In addition, there should be a correlation of the indicator concentration with the pathogen concentration and the fate and transport properties of the indicator and pathogen should be identical/similar. Unfortunately, the EPA did not evaluate the correlation of indicator with pathogen or the fate and transport characteristics of each. The EPA did however; evaluate the indicator concentration versus number of reported gastrointestinal illnesses reported by swimmers using the water bodies for primary contact recreation although they did not attempt to identify which pathogens were causing illnesses. The general consensus in the scientific community is that the majority of the illnesses were caused by enteric viruses; the anecdotal evidence supports this conclusion as the studies were done at beaches that were impacted by wastewater discharges that would typically carry human enteric viruses. The conclusions of the epidemiological studies resulted in issuance of the *Ambient Water Quality Criteria for Bacteria -1986* (EPA440/5-84-002) that recommended a water quality standard of a geometric mean of 126CFU *E. coli*/100ml (235CFU/100ml to 576CFU/100ml single sample maximum)or 33 CFU enterococcus/100mL

(61CFU/100ml to 151CFU/100ml single sample maximum) for fresh water and 35CFU enterococcus/100ml (104CFU/100ml to 500CFU/100ml single sample maximum) for marine water (based on the EPA determination that the acceptable illness rate is 8 to 19 illnesses per 1,000 swimmers). After its issuance, the EPA recommended that all States use either *E. coli* or enterococcus instead of faecal coliforms as indicators of water quality and in 2000, the Beaches Environmental Assessment and Coastal Health (BEACH) Act required States adjacent to the Great Lakes and coastal states to adopt the 1986 Standards.

8. The recommendation to change indicators was met with resistance due to the reluctance to change for a variety of reasons, including but not limited to the fact that the correlation of illnesses to indicator concentrations was not as strong as some deemed appropriate and that the epidemiological studies were carried out in waters that were impacted by wastewater treatment plant discharges. One of the major objections was that in areas that have wastewater treatment plant effluent the illness rate versus indicator concentration would be higher due to the presence of human enteric viruses in the effluent. At the time of the studies, the EPAs intention was to do additional studies to determine if indicators that were derived from various sources did in fact hold a different correlation with illness rates. However, the studies were never carried out due to funding constraints. The indicators, both *E. coli* and enterococcus are shed from virtually all warm blooded animals, e.g. cattle, pigs, deer, birds, wildlife, waterfowl, humans, pets, etc. In fact, wildlife, waterfowl and birds are major contributors of the *E. coli* and enterococcus that are found in surface waters. The issue of different sources was addressed with an EPA policy that stated a State could discount all indicator bacteria derived from nonhuman sources when making regulatory decisions. This policy was extremely important because States were in the process of developing total

maximum daily load regulations (TMDLs) to address high levels of bacteria in surface waters throughout the country and finding that *E. coli* and enterococcus were ubiquitous in the environment. Relative to the EPAs recommended standards, surface waters throughout the country are out of compliance. For example, Delaware a state with three counties, one primarily urban, one primarily agriculture and one mixed lists approximately 97% of the State's waters on the 303(d) list as impaired due to high indicator bacteria levels. Coincidently, Delaware monitors approximately 97% of its surface waters. In Oklahoma, 5,847 miles of stream segments are listed as impaired due to high enterococcus levels, 3,118 miles due to high *E. coli* levels and 2,921 miles due to high faecal coliform levels. Of the lakes assessed, 34% did not meet the primary contact recreation standards (Tenkiller Ferry Lake is not impaired by bacteria). In Oklahoma, more stream segments are listed as impaired for enterococcus than any other water quality parameter. In the IRW there are no stream segments listed as impaired by faecal coliforms, 8.6 miles listed as impaired by *E. coli* and 97.2 miles listed as impaired by enterococcus. This represents 0% of the States impairments for faecal coliforms, 0.28% of the States impairments for *E. coli* and only 1.78% of the States impairments for enterococcus (Oklahoma 2006 303(d) list). The issue of high bacteria levels is prevalent throughout Oklahoma and is in no way confined to the IRW or areas that are used for poultry production or the application of poultry litter. The bacteria levels that are seen in the IRW and throughout Oklahoma are typical of the levels seen throughout the country as evident by 303(d) listings and TMDLs that require reductions of up to and in some times greater than 90% of the indicator bacteria.

9. A TMDL is the appropriate regulatory mechanism that is in place to address impaired waters. They require monitoring, identification of the sources of a pollutant, and load allocations and pollution control strategies to remediate the problem.

10. In order to discount the nonhuman sources and determine what the sources were so that appropriate pollution control strategies (PCS) and best management practices (BMPs) could be developed, the science of microbial source tracking (MST) was developed (early/mid 1990s). MST was an extension of the principles used in track down studies such as those done by the CDC during an illness outbreak. Antibiotic resistance analysis (ARA, aka ARP – antibiotic resistance pattern) was one of the more widely used MST techniques. Initial studies reported high average rate of correct classifications (ARCC) as a measure of accuracy (using various calculation techniques including the holdout method of cross validation) and suggested that an ARCC of 60% to 70% was enough for water quality managers to base decisions on (Harwood et. al, 2000, *Classification of Antibiotic Resistance Patterns of Indicator Bacteria by Discriminant Analysis: Use in Predicting the Source of Fecal Contamination in Subtropical Waters*). Encouraged by the results of initial studies and due to the time constraints relating to the development of TMDLs and other regulatory pressures, ARA was quickly embraced by many as a mainstream technology and was widely used for MST. But as more studies were undertaken and ARA as well as other MST methods were challenged by the scientific community in method comparison studies in which known samples were given blindly to participating labs, the majority of the methods performed poorly. In both the Southern Coastal California Water Research Project (SCCWRP)/EPA study and the USGS method comparison, ARA performed very poorly and had extremely high false positive rates (39% to 100%). Dr. Harwood participated in the SCCWRP study and utilized this methodology; her lab's performance reflected this

deficiency. In addition, it was determined that the use of ARCC using techniques such as the holdout method of cross validation was not an adequate measure of the accuracy of the method (Harwood et. al., 2004, *Phenotypic library-based microbial source tracking methods: Efficacy in the California collaborative study* and Stoeckel and Harwood, 2007, *Performance, Design, and Analysis in Microbial Source Tracking Studies*). In general, library-based methods performed poorly, especially those that employed the population ecology approach to fingerprint analysis. The population ecology approach matches genetic patterns, e.g. ribotyping "fingerprints" by using mathematical algorithms to estimate the similarity between two fingerprints. In reality, two fingerprints can be very similar, often differing by only one band and be from bacteria originating from different sources. One method that is much more accurate is the molecular epidemiological approach in which only identical matches are considered to originate from the same source. This approach is used by the CDC and other regulatory agencies in track down investigations such as the determination of the source of disease outbreaks. IEH uses this analytical approach and performed the best in these method comparison studies.

11. In 2004, the EPA promulgated a rule that required the states included in the 2000 BEACH Act to adopt the 1986 bacteria standards and reversed the policy of discounting nonhuman derived bacteria indicators. However, many states that were not included in the Act were still reluctant to switch from the faecal coliform standard. There was/is still a great deal of apprehension regarding the usage of E. coli and/or enterococcus as indicators, so much so that the 2000 BEACH Act mandated the EPA to reevaluate the standards. Dr. Myoda was invited to serve in spring of 2007 as an expert in the Experts Scientific Workshop discussing the critical research and scientific needs relating to the development of a new recreational water quality standard. Issues addressed in the workshop included but were not limited to the problem that bacteria

data was not available until 24 hours after a sample was taken, there was no/weak correlations between the indicator(s) and many of the pathogens and that the correlation is variable based on the source of the indicators and the fate and transport characteristics of the indicators versus the pathogens is unclear.

12. When developing the appropriate indicator(s) to use, knowledge of the fate and transport characteristics of the indicator(s) and pathogens, both individually and as they relate to each other is critical. Individually, fate and transport is significant because only those pathogens that are present and viable in the water pose a potential public health risk to those recreating in the water. As the microbiological characteristics of each pathogen are significantly different, it is highly likely that their fate and transport characteristics will vary as well.

13. The most simplistic route of transport is direct deposition, e.g. cattle defecating in streams. Once the pathogen(s) (assumed to be carried in the feces of warm blooded mammals) is excreted over or in the water, the relevant questions are how long will the pathogen be viable and available. Indirect deposition of feces introduces many more variables affecting the fate and transport of the bacteria and or pathogen. First, the fecal properties from different mammals vary substantially. One of the primary differences (aside from pathogen and indicator density) is moisture content. Very “wet” feces is more likely than “dry” feces to introduce pathogens into the environment. After defecation, the distance from the water plays an important role as well. Driven by heavy precipitation and transported primarily via surface runoff, the organisms may be washed into the surface water by sheet flow. During this transport, they are subjected to a variety of environmental factors including but not limited to UV disinfection, predation, temperature etc. that affect the proportion that will ultimately end

up in surface water in which people are recreating. In the application of poultry litter, any indicator bacteria (as well as any other bacteria contained in the feces) are subjected to the conditions in the litter for great lengths of time prior to the application of the litter as a fertilizer/soil amendment. During this time, the composting processes along with natural die off kill a substantial portion of the bacteria. What bacteria may survive until application is then subjected to the aforementioned environmental factors and only a small portion (if any) will remain viable.

14. Resuspension from sand or sediment could also play an important role. There may be a reservoir of indicator(s) that could be reintroduced into the water column. Additional, regrowth of the indicator(s) could represent a source and confound the risk assessment/prediction.

15. Ideally, the indicator(s) chosen as the surrogate for the pathogens will have the same fate and transport characteristics of the pathogens themselves. However, since this is unlikely, it is important to know and relate the characteristics that are indicator(s) specific to the pathogens so that the measurement of the indicator can be correlated to the concentration of the viable pathogens in the water and ultimately to public health risk.

16. Lastly, when studying microbiology, it is imperative that standard methods that have been accepted by the scientific community are followed. These methods should be approved by the appropriate authority such as the EPA, Standard Methods for the Examination of Water and Wastewater, and/or AOAC, etc. This ensures that, if the tests are carried out correctly, the results are reliable and reproducible. In addition to utilizing the proper testing method, sample collection must be carried out with equal rigor and quality controls. Issues such as hold time

(normally included in the standard method) must be strictly adhered to or the results are invalid, e.g. exceeding the hold time on water samples that are being analyzed for bacteria concentrations could lead to higher counts due to regrowth. Statistically valid sampling plans must be followed; sample locations and the time the samples are taken must be randomly selected. A minimum number of samples must be taken to ensure that the testing reflects an accurate picture of the whole. Positive and negative controls must be used. Unless all these elements are included in a scientific study, the results are questionable if not invalid.

17. In reviewing the data it is apparent that standard methods were not followed in the Plaintiff's testing. In approximately 60% of the water samples, the 6 hour hold time mandated by the EPA for recreational water being tested for indicator bacteria (*E. coli*, enterococcus) was violated, in many cases by one to two days; therefore, this data is unreliable. In addition, the recreation water quality standard is based on a geometric mean of no less than 5 samples taken within 30 days, a frequency that was not maintained during the Plaintiff's study. Sampling locations were not chosen randomly. It appears that the locations that the Plaintiff's thought it most likely to find what they wanted to find were chosen. Furthermore, it appears that the timing of sample collection was not randomized either, both with respect to the time of day samples were collected and the timing relative to flow conditions. Many of the samples were taken during high flow conditions during which bacteria counts will generally be higher than average due to resuspension and runoff. Based on all of these violations of standard methodologies, we believe that the data is unreliable and is biased and skewed in favor of the Plaintiff's position.

18. The CRA report revealed egregious violations in proper sampling protocols. These violations included but were not limited to samplers walking through feces into water that they then

sampled, soil borers driven through feces and into the dirt when soil samples were taken and sampling tools not being disinfected between use. A review of the edge of field sample data reflects that the mean bacteria concentration for E. coli is 4,174 CFU/100ml, for enterococcus is 14,664 CFU/100ml, and for faecal coliforms is 6,371 CFU/100ml (see attachment A). Although there were a few samples reported to have concentrations of 1,600,000 CFU/100ml, those are atypical and represent outliers in the data set. However, even those outlying values are an order of magnitude below that of sewage influent (58,000,000 CFU *E. coli*/100ml, Miyanaga et. al, 2006, *Detection of Escherichia coli in the sewage influent by fluorescent labeled T4 phage*). In our view, the atypically high values are more consistent with samples taken in close proximity to a concentrated source of indicator bacteria, e.g. cattle feces, than with runoff samples taken from areas affected by uniformly distributed indicator bacteria such as the application of poultry litter.

19. The indicator bacteria in the waters of the IRW originate from many sources. The loading from cattle is extremely significant. Typically, cattle will excrete 15 to 35 kg of feces per day. In the summer when the majority of primary contact recreation is occurring, the initial *E. coli* concentration in the feces will be approximately 3,000,000 *CFU E. coli*/gram, however after deposition the bacteria multiply and reach levels of approximately 48,000,000 CFU *E. coli*/gram (Sinton et. al, 2007, *Survival of Indicator and Pathogenic Bacteria in Bovine Feces on Pasture).* Also in the summer months the cattle tend to congregate near and in the streams in order to cool off, increasing the possibility of direct deposition into and in close proximately of the streams. This means that each day one cow will contribute roughly 960,000,000,000 *E. coli* into the environment and with approximately 200,000 head of cattle in the IRW over 192,000,000,000,000,000 CFU *E. coli* will be introduced into the environment each day.

20. In addition to cattle, there are approximately 150,000 swine and wildlife (geese, ducks, deer, turkeys, etc) and birds that live throughout the watershed as well as the wastewater treatment plant effluent and septic system loads that are sources of indicator bacteria. Wildlife sources are a significant source of fecal material and indicator bacteria. The USGS reported that in Delaware County, Oklahoma, 45% of the *E. coli* sampled came from birds and 22% came from cattle (*Reconnaissance of the Hydrology, Water Quality, and Sources of Bacterial and Nutrient Contamination in the Ozark Plateaus Aquifer System and Cave Springs Branch of Honey Creek, Delaware County, Oklahoma, March 1999–March 2000*).

21. The presence of indicator bacteria does not mean that pathogens are present. Those that could be present include bacteria such as salmonella, campylobacter and *E. coli* O157:H7. These pathogens are carried by a variety of hosts, e.g., *E. coli* O157:H7 are primarily found in cattle, salmonella in reptiles and poultry and campylobacter in cattle, swine and poultry. Other hosts could carry these pathogens as well. The Plaintiff contends that *E. coli* O157:H7 is shed from poultry. However, there is virtually no evidence that poultry carries *E. coli* O157:H7 and the Plaintiff never tested for or found it in the litter or in the environment. Campylobacter is an organism that grows well in the conditions typically found in the digestive system. However, it does not survive well in the environment. It will die when exposed to oxygen and will also readily dehydrate and die. The Plaintiff's edge of field (EOF) sampling revealed that there was no campylobacter running off of the fields where litter had been applied[1]. Salmonella was only reported in 3 EOF samples[1], the concentrations were very low, and the source of the salmonella was not determined.

[1] No campylobacter was found in EOF water samples. Using BioSep beads, campylobacter and salmonella was reported however, using that technology the bacteria sorb onto the beads and no concentration can be determined. In addition, the reported values were all 50/bead (with the exception of one 5/bead) which raises suspicions regarding the quantification accuracy)

22. The "biomarker" that the Plaintiff claims to be poultry specific is not specific to poultry. In the extremely limited sampling of known sources used to validate this claim, the biomarker was found to be carried by ducks, geese and cattle. When retested the cattle sample came back negative and the explanation given by Dr. Harwood was that it was most likely due to contamination in the laboratory. If contamination was occurring in the laboratory the reliability of all the test results are suspect except the duck and goose positive samples which were verified to be correct.

23. Absence of proof is not proof of absence. Only 24 cattle manure composites, 2 swine manure composites, 10 duck and 10 goose manure composites, 3 septic and 3 wwtp samples were tested to validate the specificity of the biomarker. Virtually all of the sources of the indicator bacteria in the IRW were not tested, e.g. birds, deer, wild turkeys, pets, wildlife, etc. Additionally, the manure composites were taken from 10 "patties" so it is impossible to know if one in ten or all ten in ten carried the biomarker. If only one in ten carried the biomarker, diluting it with 9 other patties may have reduced the concentration below the method detection limit. When the samples were taken, locations were not randomly selected and the geographic variability was not captured. It is very probable that the bacterial communities of animals living in close proximity to one another will be similar therefore, in order to capture a more representative sample of the watershed, 10 patties should be taken from 10 different farms, not

10 from the same farm (Hartel et. al, 2007, *Geographic sharing of ribotype patterns in enterococcus faecalis for bacteria source tracking*).

24. The "poultry biomarker" MST method is not a standard method nor has it been peer reviewed or third party tested, making it at best a research method and not one that can or should be used for any regulatory action(s) or used to draw conclusions about the sources of indicator bacteria in the IRW (or anywhere else).

25. The method is based on the amplification of a particular genetic sequence that may or may not be from a live organism. The polymerase chain reaction (PCR) cannot differentiate between live or dead organisms. DNA can persist for long periods of time in the environment, creating positive PCR results long after the indicator or pathogen has been introduced into the environment and has died. Pathogens, in this case salmonella and campylobacter need to be alive to be infectious.

26. The genetic sequence used as the biomarker is a portion of the 16S rRNA gene. The known bacteria that has the closest sequence to this fragment is *Brevibacterium avium*. *Brevibacterium avium* was first identified and isolated from bumble-foot lesions in domestic fowl in 1999. *B. avium* can be cultured and is differentiated from other Brevibaterium species by both its genetic sequence and phenotypical traits e.g., temperature that it grows, utilization of arabinose, etc. It is perplexing that no attempt to culture this "new" bacteria species that the Plaintiff claims to have discovered was carried out. There is no evidence that this "new" organism is viable or pathogenic. Dr. Harwood stated that it is close to the pathogenic, *B. casei*, although genetic analysis indicates that it is much closer to *B. avium*. Being in the same genus as a pathogen does

not mean that it will be a pathogen, e.g. the majority of E. coli is nonpathogenic although the nearly identical *E. coli* O157:H7 is highly pathogenic.

27. The Plaintiff claims that the levels of biomarker can be used to quantify the indicator bacteria originating from poultry. However, when developing the quantitative aspect of this assay, negative values were reported for the amount of DNA present. It is impossible to have negative amounts of DNA. Therefore the standard curves used in quantification cannot be correct and the quantitative values reported by the Plaintiff are also incorrect.

28. There is no correlation between the amount of the biomarker and the indicator organism concentration in the litter (see attachment 3). Assuming that all the other technical issues surrounding this new test could be overcome, without a correlation between indicator concentration and biomarker concentration in the litter it is impossible to extrapolate the amount of indicator bacteria originating from poultry in the waters of the IRW.

29. There is no public health linkage between the biomarker and illness rates. No epidemiological studies have been conducted to determine if there is a correlation between these two parameters.

30. Indicator bacteria are ubiquitous and originate from multiple sources in the IRW. Major contributors include cattle, swine and wildlife. The new “biomarker” that the Plaintiffs claim proves that poultry is the primary source of indicator bacteria is not specific therefore, it does not support that conclusion. In addition, there is no correlation between it and the indicator bacteria in the litter so it cannot be used as a quantitative tool. Based on the data that we have

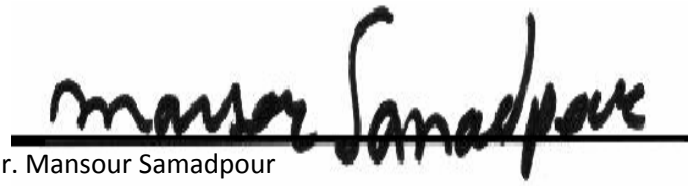
reviewed, there is no evidence that poultry is the major contributor of indicator bacteria or that there is an imminent public health threat in the IRW.

I declare under penalty of perjury that the foregoing is true and correct.

Executed on February 8, 2008

Sam Myoda

Dr. Samuel P. Myoda



Dr. Mansour Samadpour